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1. A method for characterizing disease activity in a systemic lupus erythematosus patient (SLE), comprising:

(a) obtaining a dataset associated with a blood, serum, plasma or urine sample from the patient, wherein the dataset comprises data representing the level of one or more biomarkers in the blood, serum, plasma or urine sample from each of (b) to (g);

(b) assessing the dataset for a presence or an amount of protein expression of at least one innate serum or plasma mediator biomarker selected from: IL-1α, IL-1β, IL-1RA, IFN-α, IL-12p'70, IL-6, and IL-23p19;

(c) assessing the dataset for a presence or an amount of protein expression of at least one adaptive serum or plasma mediator biomarker selected from: IL-2, IFN-γ, IL-5, IL-13, IL-17A, IL-21, IL-10, and TGF-β;

(d) assessing the dataset for a presence or an amount of at least one chemokine/adhesion molecule biomarker selected from: IL-8/CXCL8, IP-10/CXCL10, MIG/CXCL9, MIP-1α/CCL3, MIP-1β/CCL4, MCP-1/CCL2, MCP-3/CCL7, and ICAM-1;

(e) assessing the dataset for a presence or an amount of at least one soluble TNF superfamily biomarker selected from: TNFRI, TNFRII, TRAIL, TWEAK, CD40L/CD154, BLyS, and APRIL;

(f) assessing the dataset for a presence or an amount of the inflammatory mediator biomarker SCF;

(g) assessing the dataset for a presence or an amount at least one SLE-associated autoantibody specificity biomarker selected from: dsDNA, chromatin, RiboP, Ro/SSA, La/SSB, Sm, SmRNP, and RNP; and

(h) calculating a Lupus Disease Activity Immune Index (LDAII) score.

2. The method of claim **1**, wherein two or more of each of the innate, adaptive, chemokine/adhesion molecule, soluble TNF superfamily, and SLE-associated autoantibody specificity biomarkers and the inflammatory mediator biomarker are used in the calculation of the LDAII.

3. The method of claim **1**, wherein the dataset is: log transformed; standardized;

weighted by Spearman r correlation to the autoantibody specificities in the second dataset, and a summation of soluble protein markers equals an LDAII score.

4. The method of claim **1**, wherein performance of the at least one immunoassay comprises: obtaining the first sample, wherein the first sample comprises the protein markers; contacting the first sample with a plurality of distinct reagents; generating a plurality of distinct complexes between the reagents and markers; and detecting the complexes to generate the data.

5. The method of claim **1**, wherein the at least one immunoassay comprises a multiplex assay.

6. (canceled)

7. (canceled)

8. The method of claim **1**, further comprising administering a treatment to the patient prior to reaching clinical disease classification after determining that the patient has the prognosis for transitioning to classified SLE, wherein the treatment comprises at least one of: hydroxychloroquine (HCQ), belimumab, a nonsteroidal anti-inflammatory drug, a steroid, or a disease-modifying anti-rheumatic drug (DMARD).

9. A method of evaluating disease activity and progression of Systemic Lupus Erythematosus (SLE) clinical disease in a patient comprising:

obtaining a blood, serum, plasma or urine sample from the patient;

performing at least one immunoassay on a sample from the patient to generate a dataset comprising at least one biomarker from each of (1) to (6):

(1) assessing the dataset for a presence or an amount of protein expression of at least one innate serum or plasma mediator biomarker selected from: IL-1α, IL-1β, IL-1RA, IFN-α, IL-12p'70, IL-6, and IL-23p19;

(2) assessing the dataset for a presence or an amount of protein expression of at least one adaptive serum or plasma mediator biomarker selected from: IL-2, IFN-γ, IL-5, IL-13, IL-17A, IL-21, IL-10, and TGF-β;

(3) assessing the dataset for a presence or an amount of at least one chemokine/adhesion molecule biomarker selected from: IL-8/CXCL8, IP-10/CXCL10, MIG/CXCL9, MIP-1α/CCL3, MIP-1β/CCL4, MCP-1/CCL2, MCP-3/CCL7, and ICAM-1;

(4) assessing the dataset for a presence or an amount of at least one soluble TNF superfamily biomarker selected from: TNFRI, TNFRII, TRAIL, TWEAK, CD40L/CD154, BLyS, and APRIL;

(5) assessing the dataset for a presence or an amount of the inflammatory mediator biomarker SCF; and